

CLAIMS

We claim at least the following:

- 1 1. A method of performing nanopore data analysis, comprising:
2 providing a sample including target polymers and non-target polymers
3 and a nanopore device, wherein the target polymers and non-target polymers
4 are selected from polynucleotides and polypeptides;
5 introducing the sample to the nanopore device;
6 generating nanopore data points corresponding to each target polymer
7 and each non-target polymer traversing an aperture of the nanopore;
8 forming a distribution pattern of the nanopore data points; and
9 analyzing a distribution of polymer data points in the distribution
10 pattern.
- 1 2. The method of claim 1, wherein the distribution pattern includes at least one
2 data cluster, and wherein analyzing includes analyzing the distribution of
3 target polynucleotide data points within the at least one data cluster.
- 1 3. The method of claim 2, further comprising:
2 comparing the distribution of the target polynucleotide data points
3 between two data clusters to a phosphorylation state standard distribution.
- 1 4. The method of claim 3, further comprising:
2 determining a ratio of phosphorylated target polynucleotide to non-
3 phosphorylated target polynucleotides.

1 5. The method of claim 2, further comprising:

2 determining a ratio of phosphorylated target polynucleotide to non-
3 phosphorylated target polynucleotides.

1 6. The method of claim 1, further comprising:

2 comparing a density distribution of the target polynucleotide data
3 points to a chemical integrity standard density distribution, wherein a change
4 in the density distribution of target polynucleotide data points as compared to
5 the chemical integrity standard density distribution indicates that the chemical
6 integrity of the target polynucleotides in the sample is different than a
7 chemical integrity for which the chemical integrity standard density
8 distribution was prepared.

1 7. The method of claim 6, further comprising:

2 determining the density of target polynucleotide data points in a
3 defined area; and
4 comparing the density of the target polynucleotide data points to a
5 chemical integrity standard density distribution for the defined area.

- 1 8. The method of claim 6, further comprising:
2 determining the density of target polynucleotide data points in a
3 defined area;
4 comparing the density of the target polynucleotide data points to a
5 density of the target polynucleotide data points of at least two other samples
6 including target polynucleotides and non-target polynucleotides; and
7 ranking the samples based on the density of the target polynucleotide
8 data points.
- 1 9. The method of claim 6, further comprising:
2 determining a cluster score for the target polynucleotide data points in
3 a defined area; and
4 comparing the cluster score for the target polynucleotide data points to
5 a cluster score for a chemical integrity standard density distribution for the
6 defined area.
- 1 10. The method of claim 2, further comprising:
2 analyzing the distribution of the non-target polynucleotide data points.
- 1 11. The method of claim 10, wherein distribution of non-target polynucleotide
2 data points outside of the at least one cluster indicates that non-target
3 polynucleotides have a different length than the target polynucleotides.

1 12. The method of claim 10, wherein distribution of non-target polynucleotide
2 data points outside of the at least one cluster indicates that the non-target
3 polynucleotides have the same length as the target polynucleotide but the
4 sequence of the non-target polynucleotide and target polynucleotide is not the
5 same.

1 13. The method of claim 10, further comprising:
2 determining a ratio between the target polynucleotide data points and
3 the non-target polynucleotide data points.

1 14. The method of claim 1, wherein the failure of polymer data points to
2 form at least one cluster indicates that the target polymers in the sample
3 represent less than a calibration specified fraction of the total polymers in the
4 sample.

1 15. A system for performing nanopore data analysis, comprising:
 2 a nanopore system including a nanopore device and a nanopore data
 3 analysis system, the nanopore device having a structure having an aperture, the
 4 nanopore data analysis system operative to:
 5 generate nanopore data points corresponding to each target
 6 polymer and each non-target polymer traversing the aperture of the
 7 nanopore structure;
 8 form a distribution pattern of the data points; and
 9 analyze a distribution of target polymer data points in the
 10 distribution pattern.

1 16. The system of claim 15, wherein the nanopore data analysis system is further
 2 operative to analyze the distribution of the non-target polynucleotide data
 3 points.

1 17. The system of claim 16, wherein the nanopore data analysis system is further
 2 operative to determine a ratio between the target polynucleotide data points
 3 and the non-target polynucleotide data points.

1 18. The system of claim 18, wherein the distribution pattern includes at least one
 2 data cluster and wherein the nanopore data analysis system is further operative
 3 to:
 4 analyze of the distribution of target polynucleotide data points between
 5 the two data clusters;
 6 comparing the distribution of the target polynucleotide data points
 7 between the two data clusters to a phosphorylation state standard distribution;
 8 and
 9 determine a ratio of phosphorylated target polynucleotide to non-
 10 phosphorylated target polynucleotides.

1 19. The system of claim 15, wherein the nanopore data analysis system is further
 2 operative to:
 3 determine a cluster score for the target polynucleotide data points in a
 4 defined area; and
 5 compare the cluster score for the target polynucleotide data points to a
 6 cluster score for a chemical integrity standard density distribution for the
 7 defined area in a distribution of a target polynucleotide standard.

1 20. The system of claim 15, wherein the nanopore data analysis system is stored
 2 on a computer-readable medium.

1 22. The system of claim 15, further comprising:
 2 means for analyzing the distribution of target polynucleotide data
 3 points in the distribution pattern